

**In the Claims:**

Please amend claim 28 as follows:

28. (Once Amended) An oligonucleotide in accordance with claim 18, wherein said oligonucleotide is a member selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22.

**REMARKS**

A marked up copy of amended claim 28 is provided as an appendix entitled "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**" As a convenience to the Examiner, a complete set of the Claims, as amended herein, is also attached to this Amendment as an appendix entitled "**PENDING CLAIMS WITH ENTRY OF THE AMENDMENT**".

*marked  
5/17/02*

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-22, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

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If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

**In the Specification:**

Paragraph (Table 2) beginning at line 1 of page 39 has been amended as follows:

**Table 2**

*Relative quantum yields of oligonucleotides containing 6MAP or DMAP*

SEQ ID NO:	Sequence (5' → 3')	w/6MAP	Q <sub>rel</sub>
1	gtg tgg Faa atc tct agc agt	PTR21	0.010
2	gtg tgg aaa Ftc tct agc agt	PTR22	0.020
3	gtg tgg aaa atc tct Fgc agt	PTR23	0.018
4	act gct Fga gat ttt cca cac	PTR24	
5	act gct agF gat ttt cca cac	PTR25	0.011
6	act gct agc cFt ttt cca cac	PTR28	0.041
7	att cca caa Fgc cgt gtc a	HP21	0.010
8	aga ggt gtc cFc ctg tgg aga	HP22	<0.01
9	aga ggt gta cFa gtg tgg aga	HP23	0.012
10	aga ggt gta aFa atg tgg aga	HP24	<0.01
	<b>Sequence (5' → 3')</b>	<b>w/DMAP</b>	<b>Q<sub>rel</sub></b>
11	gtg tgg Faa atc tct agc agt	PTR31	0.023
12	gtg tgg aaa Ftc tct agc agt	PTR32	0.022
13	gtg tgg aaa atc tct Fgc agt	PTR33	0.01
14	act gct Fga gat ttt cca cac	PTR34	0.012
15	act gct agF gat ttt cca cac	PTR35	0.017
16	act gct aga gFt ttt cca cac	PTR36	0.019
17	act gct aga gat ttt ccF cac	PTR37	0.11
18	act gct agc cFt ttt cca cac	PTR38	0.11
19	att cca caa Fgc cgt gtc a	HP31	0.02
20	aga ggt gtc cFc ctg tgg aga	HP32	<0.01
21	aga ggt gta cFa gtg tgg aga	HP33	0.02
22	aga ggt gta aFa atg tgg aga	HP34	<0.01

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